



IFWO

## RAW SEQUENCE LISTING

DATE: 09/01/2004

PATENT APPLICATION: US/10/804,457

TIME: 12:51:43

Input Set : N:\Cr3\RULE60\10804457.raw

Output Set : N:\CRF4\09012004\J804457.raw

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1 <110> APPLICANT: Friddle, Carl Johan
2   Hilbun, Erin
3 <120> TITLE OF INVENTION: Novel Human Proteases and Polynucleotides Encoding the
4   Same
5 <130> FILE REFERENCE: LEX-0219-USA
6 <140> CURRENT APPLICATION NUMBER: US/10/804,457
7 <141> CURRENT FILING DATE: 2004-03-19.
8 <150> PRIOR APPLICATION NUMBER: US/10/217,774
9 <151> PRIOR FILING DATE: 2002-08-12
10 <150> PRIOR APPLICATION NUMBER: US/09/930,872
11 <151> PRIOR FILING DATE: 2001-08-14
12 <150> PRIOR APPLICATION NUMBER: US 60/225,852
13 <151> PRIOR FILING DATE: 2000-08-16
14 <160> NUMBER OF SEQ ID NOS: 5
15 <170> SOFTWARE: FastSEQ for Windows Version 4.0
17 <210> SEQ ID NO: 1
18 <211> LENGTH: 1476
19 <212> TYPE: DNA
20 <213> ORGANISM: homo sapiens
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24   agcgtcccgc gtccctctcc acccgcgagg cggcggggct ggatggaaaa gggcgaatat      180
25   gacctggtct ctgcctacga ggttgaccac aggggcgatt acgtgtccca tgaaatcatg      240
26   caccatcagc ggcggagaag agcagtggcc gtgtccgagg ttgagtctct tcaccttcgg      300
27   ctgaaaggct ccaggcacga cttccacgtg gatctgagga cttccagcag cctagtggct      360
28   cctggcttta ttgtgcagac gttgggaaag acaggcacta agtctgtgca gactttaccg      420
29   ccagaggact tctgtttcta tcaaggctct ttgcgatcac acagaaactc ctcagtggcc      480
30   ctttcaacct gccaaaggctt gtcaggcatg atacgaacag aagaggcaga ttacttccta      540
31   aggccacttc cttcacacct ctcatggaaa ctgcgcagag ctgcccagg cagctcgcca      600
32   tcccacgtac tgtacaagag atccacagag ccccatgtct ctggggccag tgaggtcctg      660
33   gtgacctcaa ggacatggga gctggcacat caaccctgc acagcagcga ccttcgcctg      720
34   ggactgccac aaaagcagca tttctgtgga agacgcaaga aatacatgcc ccagcctccc      780
35   aaggaagacc tcttcatctt gccagatgag tataagtctt gcttacggca taagcgctct      840
36   cttctgaggt cccatagaaa tgaagaactg aacgtggaga ccttggtggt ggtcgacaaa      900
37   aagatgatgc aaaacctagg ccatgaaaat atcaccacct acgtgtcac gatactcaac      960
38   atggtatctg ctttattcaa agatggaaca ataggaggaa acatcaacat tgcaattgta     1020
39   ggtctgattc ttctagaaga tgaacagcca ggactggtga taagtcacca cgcagaccac     1080
40   accttaagta gcttctgcca gtggcagctt ggattgatgg ggaagatgg gactcgtcat     1140
41   gaccacgcca tcttactgac tggctctgat atatgttctt ggaagaatga gccctgtgac     1200
42   actttgggat ttgcacccat aagtggaatg tgtagtaaat atcgagctg cacgattaat     1260
43   gaagatacag gtcttgagct ggccttcacc attgcccatt agtctggaca caactttggc     1320
44   atgattcatg atggagaagg gaacatgtgt aaaaagtcgg agggcaacat catgtcccct     1380

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45      acattggcag gacgcaatgg agtcttctcc tggtcaccct gcagccgcca gatatctacac      1440
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49 <211> LENGTH: 491
50 <212> TYPE: PRT
51 <213> ORGANISM: homo sapiens
52 <400> SEQUENCE: 2
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55      Leu Leu Ala Gln Val Ala Glu Gln Ala Pro Ala Cys Ala Met Gly Pro
56      20          25          30
57      Ala Ala Ala Ala Pro Gly Ser Pro Ser Val Pro Arg Pro Pro Pro Pro
58      35          40          45
59      Ala Glu Arg Pro Gly Trp Met Glu Lys Gly Glu Tyr Asp Leu Val Ser
60      50          55          60
61      Ala Tyr Glu Val Asp His Arg Gly Asp Tyr Val Ser His Glu Ile Met
62      65          70          75          80
63      His His Gln Arg Arg Arg Ala Val Ala Val Ser Glu Val Glu Ser
64      85          90          95
65      Leu His Leu Arg Leu Lys Gly Ser Arg His Asp Phe His Val Asp Leu
66      100         105         110
67      Arg Thr Ser Ser Ser Leu Val Ala Pro Gly Phe Ile Val Gln Thr Leu
68      115         120         125
69      Gly Lys Thr Gly Thr Lys Ser Val Gln Thr Leu Pro Pro Glu Asp Phe
70      130         135         140
71      Cys Phe Tyr Gln Gly Ser Leu Arg Ser His Arg Asn Ser Ser Val Ala
72      145         150         155         160
73      Leu Ser Thr Cys Gln Gly Leu Ser Gly Met Ile Arg Thr Glu Glu Ala
74      165         170         175
75      Asp Tyr Phe Leu Arg Pro Leu Pro Ser His Leu Ser Trp Lys Leu Gly
76      180         185         190
77      Arg Ala Ala Gln Gly Ser Ser Pro Ser His Val Leu Tyr Lys Arg Ser
78      195         200         205
79      Thr Glu Pro His Ala Pro Gly Ala Ser Glu Val Leu Val Thr Ser Arg
80      210         215         220
81      Thr Trp Glu Leu Ala His Gln Pro Leu His Ser Ser Asp Leu Arg Leu
82      225         230         235         240
83      Gly Leu Pro Gln Lys Gln His Phe Cys Gly Arg Arg Lys Lys Tyr Met
84      245         250         255
85      Pro Gln Pro Pro Lys Glu Asp Leu Phe Ile Leu Pro Asp Glu Tyr Lys
86      260         265         270
87      Ser Cys Leu Arg His Lys Arg Ser Leu Leu Arg Ser His Arg Asn Glu
88      275         280         285
89      Glu Leu Asn Val Glu Thr Leu Val Val Val Asp Lys Lys Met Met Gln
90      290         295         300
91      Asn His Gly His Glu Asn Ile Thr Thr Tyr Val Leu Thr Ile Leu Asn
92      305         310         315         320
93      Met Val Ser Ala Leu Phe Lys Asp Gly Thr Ile Gly Gly Asn Ile Asn
94      325         330         335

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Input Set : N:\Crif3\RULE60\10804457.raw

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95   Ile Ala Ile Val Gly Leu Ile Leu Leu Glu Asp Glu Gln Pro Gly Leu
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97   Val Ile Ser His His Ala Asp His Thr Leu Ser Ser Phe Cys Gln Trp
98           355                     360                     365
99   Gln Ser Gly Leu Met Gly Lys Asp Gly Thr Arg His Asp His Ala Ile
100          370                     375                     380
101   Leu Leu Thr Gly Leu Asp Ile Cys Ser Trp Lys Asn Glu Pro Cys Asp
102          385                     390                     395                     400
103   Thr Leu Gly Phe Ala Pro Ile Ser Gly Met Cys Ser Lys Tyr Arg Ser
104           405                     410                     415
105   Cys Thr Ile Asn Glu Asp Thr Gly Leu Gly Leu Ala Phe Thr Ile Ala
106           420                     425                     430
107   His Glu Ser Gly His Asn Phe Gly Met Ile His Asp Gly Glu Gly Asn
108           435                     440                     445
109   Met Cys Lys Lys Ser Glu Gly Asn Ile Met Ser Pro Thr Leu Ala Gly
110          450                     455                     460
111   Arg Asn Gly Val Phe Ser Trp Ser Pro Cys Ser Arg Gln Tyr Leu His
112          465                     470                     475                     480
113   Lys Phe Leu Arg Ser Val Lys Met Pro Ala Leu
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116 &lt;210&gt; SEQ ID NO: 3

117 &lt;211&gt; LENGTH: 3675

118 &lt;212&gt; TYPE: DNA

119 &lt;213&gt; ORGANISM: homo sapiens

120 &lt;400&gt; SEQUENCE: 3

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122   gtggccgagc aggcacctgc gtgcgccatg ggacccgcag cggcagcgcc tgggagcccc      120
123   agcgtcccgc gtcctcctcc acccgcgag cggccgggct ggatggaaaa gggcgaatat      180
124   gacctggtct ctgcctacga ggttgaccac agggggcgatt acgtgtccca tgaaatcatg      240
125   caccatcagc ggcgagagaag agcagtggcc gtgtccgagg ttgagtctct tcaccttcgg      300
126   ctgaaaggct ccaggcacga cttccacgtg gatctgagga cttccagcag cctagtggct      360
127   cctggcttta ttgtgcagac gttgggaaag acaggcacta agtctgtgca gactttaccg      420
128   ccagaggact tctgtttcta tcaaggctct ttgcgatcac acagaaactc ctcagtggcc      480
129   ctttcaacct gccaaggctt gtcaggcatg atacgaacag aagaggcaga ttacttccta      540
130   aggccacttc cttcacacct ctcatggaaa ctcggcagag ctgcccagg cagctcgcca      600
131   tcccacgtac tgtacaagag atccacagag ccccatgctc ctggggccag tgaggctctg      660
132   gtgacctcaa ggacatggga gctggcacat caaccctgc acagcagcga ctttcgctg      720
133   ggactgccac aaaagcagca tttctgtgga agacgcaaga aatacatgcc ccagcctccc      780
134   aaggaagacc tcttcatctt gccagatgag tataagtctt gcttacggca taagcgctct      840
135   cttctgaggt cccatagaaa tgaagaactg aacgtggaga ccttggtggt ggtcgacaaa      900
136   aagatgatgc aaaaccatgg ccatgaaaat atcaccacct acgtgctcac gatactcaac      960
137   atggtatctg ctttattcaa agatggaaca ataggaggaa acatcaacat tgcaattgta     1020
138   ggtctgattc ttctagaaga tgaacagcca ggactggtga taagtcacca cgcagaccac     1080
139   accttaagta gcttctgcca gtggcagtct ggattgatgg ggaaagatgg gactcgctcat     1140
140   gaccacgcca tcttactgac tggctctggat atatgttctt ggaagaatga gccctgtgac     1200
141   actttgggat ttgcacccat aagtggaatg tgtagtaaat atcgcagctg cagattaat     1260
142   gaagatacag gtcttggaact ggccctcacc attgcccatt agtctggaca caactttggc     1320
143   atgattcatg atggagaagg gaacatgtgt aaaaagtcct agggcaacat catgtcccct     1380
144   acattggcag gacgcaatgg agtcttctcc tggtcacct gcagccgcca gtatctacac     1440

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145 aaattttctaa gcaccgctca agctatctgc cttgctgac agccaaagcc tgtgaaggaa 1500
146 tacaagtatc ctgagaaatt gccaggagaa ttatatgatg caaacacaca gtgcaagtgg 1560
147 cagttcggag agaaagccaa gctctgcatg ctggacttta aaaaggacat ctgtaaagcc 1620
148 ctgtggtgcc atcgatttgg aaggaaatgt gagactaaat ttatgccagc agcagaagcc 1680
149 acaattttgtg ggcattgacat gtggtgcccgg ggaggacagt gtgtgaaata tggatgatgaa 1740
150 ggccccaagc ccacccatgg ccaactggtcg gactggtctt cttggtcccc atgctccagg 1800
151 acctgctggag ggggagtatc tcataggagt cgctctgca ccaaccccaa gccatcgcat 1860
152 ggagggaagt tctgtgaggg ctccactcgc actctgaagc tctgcaacag tcagaaatgt 1920
153 ccccgggaca gtgttgactt ccgtgctgct cagtgtgccg agcacaacag cagacgattc 1980
154 agaggcgccg actacaagtg gaagccttac actcaagtag aagatcagga cttatgcaaa 2040
155 ctctactgta tcgcagaagg atttgatttc ttcttttctt tgtcaaataa agtcaaagat 2100
156 gggactccat gctcggagga tagccgtaat gtttgtatag atgggatatg tgagagagtt 2160
157 ggatgtgaca atgtccttgg atctgatgct gttgaagacg tctgtggggg gtgtaacggg 2220
158 aataactcag cctgcacgat tcacaggggt ctctacacca agcaccacca caccaaccag 2280
159 tattatcaca tggtcaccat tccttctgga gcccgaggta tccgcatcta tgaaatgaac 2340
160 gtctctacct cctacatttc tgtgcgcaat gccctcagaa ggtactacct gaatgggcac 2400
161 tggaccgtgg actggcccgg ccggtacaaa ttttcgggca ctactttcga ctacagacgg 2460
162 tcctataatg agcccagaaa cttaatcgct actggaccaa ccaacgagac actgattgtg 2520
163 gagctgctgt ttcaggggaag gaacccgggt gttgcctggg aatactccat gcctcgcttg 2580
164 gggaccgaga agcagccccc tgcccagccc agctacactt bggccatcgt gcgctctgag 2640
165 tgctccgtgt cctgcggagg gggacagatg accgtgagag agggctgcta cagagacctg 2700
166 aagtttcaag taaatatgtc cttctgcaat cccaagacac gacctgtcac ggggctggtg 2760
167 ccttgcaaag tatctgcctg tcctcccagc tggctcgtgg ggaactggag tgctgcagt 2820
168 cggacgtgtg gcgggggtgc ccagagccgc cccgtgcagt gcacacggcg ggtgcactat 2880
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180 cccattgcag agaagaaaga tgcttctgc aaagactact tccactggtg ctacctggta 3600
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186 <212> TYPE: PRT
187 <213> ORGANISM: homo sapiens
188 <400> SEQUENCE: 4
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191 Leu Leu Ala Gln Val Ala Glu Gln Ala Pro Ala Cys Ala Met Gly Pro
192 20 25 30
193 Ala Ala Ala Ala Pro Gly Ser Pro Ser Val Pro Arg Pro Pro Pro
194 35 40 45

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195   Ala Glu Arg Pro Gly Trp Met Glu Lys Gly Glu Tyr Asp Leu Val Ser
196       50                      55                      60
197   Ala Tyr Glu Val Asp His Arg Gly Asp Tyr Val Ser His Glu Ile Met
198   65                      70                      75                      80
199   His His Gln Arg Arg Arg Arg Ala Val Ala Val Ser Glu Val Glu Ser
200                      85                      90                      95
201   Leu His Leu Arg Leu Lys Gly Ser Arg His Asp Phe His Val Asp Leu
202                      100                     105                     110
203   Arg Thr Ser Ser Ser Leu Val Ala Pro Gly Phe Ile Val Gln Thr Leu
204                      115                     120                     125
205   Gly Lys Thr Gly Thr Lys Ser Val Gln Thr Leu Pro Pro Glu Asp Phe
206                      130                     135                     140
207   Cys Phe Tyr Gln Gly Ser Leu Arg Ser His Arg Asn Ser Ser Val Ala
208   145                      150                     155                     160
209   Leu Ser Thr Cys Gln Gly Leu Ser Gly Met Ile Arg Thr Glu Glu Ala
210                      165                     170                     175
211   Asp Tyr Phe Leu Arg Pro Leu Pro Ser His Leu Ser Trp Lys Leu Gly
212                      180                     185                     190
213   Arg Ala Ala Gln Gly Ser Ser Pro Ser His Val Leu Tyr Lys Arg Ser
214                      195                     200                     205
215   Thr Glu Pro His Ala Pro Gly Ala Ser Glu Val Leu Val Thr Ser Arg
216                      210                     215                     220
217   Thr Trp Glu Leu Ala His Gln Pro Leu His Ser Ser Asp Leu Arg Leu
218   225                      230                     235                     240
219   Gly Leu Pro Gln Lys Gln His Phe Cys Gly Arg Arg Lys Lys Tyr Met
220                      245                     250                     255
221   Pro Gln Pro Pro Lys Glu Asp Leu Phe Ile Leu Pro Asp Glu Tyr Lys
222                      260                     265                     270
223   Ser Cys Leu Arg His Lys Arg Ser Leu Leu Arg Ser His Arg Asn Glu
224                      275                     280                     285
225   Glu Leu Asn Val Glu Thr Leu Val Val Val Asp Lys Lys Met Met Gln
226                      290                     295                     300
227   Asn His Gly His Glu Asn Ile Thr Thr Tyr Val Leu Thr Ile Leu Asn
228   305                      310                     315                     320
229   Met Val Ser Ala Leu Phe Lys Asp Gly Thr Ile Gly Gly Asn Ile Asn
230                      325                     330                     335
231   Ile Ala Ile Val Gly Leu Ile Leu Leu Glu Asp Glu Gln Pro Gly Leu
232                      340                     345                     350
233   Val Ile Ser His His Ala Asp His Thr Leu Ser Ser Phe Cys Gln Trp
234                      355                     360                     365
235   Gln Ser Gly Leu Met Gly Lys Asp Gly Thr Arg His Asp His Ala Ile
236                      370                     375                     380
237   Leu Leu Thr Gly Leu Asp Ile Cys Ser Trp Lys Asn Glu Pro Cys Asp
238   385                      390                     395                     400
239   Thr Leu Gly Phe Ala Pro Ile Ser Gly Met Cys Ser Lys Tyr Arg Ser
240                      405                     410                     415
241   Cys Thr Ile Asn Glu Asp Thr Gly Leu Gly Leu Ala Phe Thr Ile Ala
242                      420                     425                     430
243   His Glu Ser Gly His Asn Phe Gly Met Ile His Asp Gly Glu Gly Asn

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Input Set : N:\Crf3\RULE60\10804457.raw  
Output Set: N:\CRF4\09012004\J804457.raw

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VERIFICATION SUMMARY

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TIME: 12:51:44

Input Set : N:\Crf3\RULE60\10804457.raw

Output Set: N:\CRF4\09012004\J804457.raw

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